GM nucleic - nucleic search, using sw model

GenCore version 5.1.4_p5_4578
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Run on: May 2, 2003, 14:33:45 ; Search time 83775 Seconds
                                        (without alignments)
                                        2.679 Million cell updates/sec

Title: us-09-673-476-1
Perfect score: 12732
Sequence: 1 acctgcgcttgcagagatca.......... gtcggtgctggttggctcgc 12732

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 8815365 residues

Total number of hits satisfying chosen parameters: 4

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :   1: *gbk:*
               1: /home/sdavid/sdavid-tmp/may03/chakrabarti476/AL123456.gbk:*
               2: /home/sdavid/sdavid-tmp/may03/chakrabarti476/AE000516.gbk:*

               Pred. No. is the number of results predicted by chance to have a
               score greater than or equal to the score of the result being printed,
               and is derived by analysis of the total score distribution.

SUMMARIES

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Result          %        Query
 No.   Score  Match Length DB   ID          Description
-----  -----  ----- ------ --   --          -----------
   1   12732  100.0  4411529  1  AL123456   ACCESSION:AL123456
 2  12715.7   99.9  4403886  2  AE000516   ACCESSION:AE000516
c  3   484.999   3.8  4403886  2  AE000516   ACCESSION:AE000516
c  4   483.599   3.8  4411529  1  AL123456   ACCESSION:AL123456
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ALIGNMENTS

RESULT 1
LOCUS   AL123456 4411529 bp   circular BCT   07-JUL-1998
DEFINITION   Mycobacterium tuberculosis complete genome.
ACCESSION   AL123456
VERSION   AL123456
KEYWORDS   .
SOURCE   Mycobacterium tuberculosis.
  ORGANISM   Mycobacterium tuberculosis
             Bacteria; Firmicutes; Actinomycetes; Mycobacterium.
             Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 4411529)
  AUTHORS   Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,
             Harris,D., Gordon,S.V., Eiglmeier,K., Gas,S., Barry III,C.E.,
             Tekaia,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T.,
             Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentles,S.,
             Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J.,
             Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A.,
             Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S.,
             Squares,R., Squares,S., Sulston,J.E., Taylor,K., Whitehead,S. and
             Barrell,B.G.
  TITLE   Deciphering the biology of Mycobacterium tuberculosis from the

JOURNAL   Nature 393 (6685), 537-544 (1998)
MEDLINE   98295987
REFERENCE   2 (bases 1 to 4411529)
  AUTHORS   Parkhill,J.
  TITLE   Direct Submission
  JOURNAL   Submitted (11-JUN-1998) submitted on behalf of the Mycobacterium
             tuberculosis Sequencing and Mapping Group, Sanger Centre, Wellcome
             Trust Genome Campus, Hinxton, Cambridge CB10 1SA United Kingdom
             Molecular Bacteriologie, Institut Pasteur, 28 rue du Docteur Roux,
             75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
FEATURES   Location/Qualifiers
     source   1..4411529
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                     /db_xref="taxon:1773"
     gene   1..1524
                     /gene="dnaA"
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                     /db_xref="EMBL:3261512"
     CDS   1..1524
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                     /note="Rv0001, (MTV029.01), len: 507, dnaA, chromosomal
                     replication initiator protein, identical to TR:O69595
                     (EMBL:X92504) and highly similar to many eg. DNAA_ECOLI
                     P03004 chromosomal replication initiator protein (467 aa),
                     fasta scores: opt 986 z-score 1154.5 E(): 0; 43.2%
                     identity in 469 aa overlap. Contains PS00017 DnaA
                     ATP/GTP-binding site motif A (P-loop) and PS01008 DnaA
                     protein signature. Note that the first base of this gene
                     has been taken as base 1 of the M. tuberculosis H37Rv
                     genomic sequence."
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                     EGKEICEEPFHIFNILHINAKG.V:SSDKRPKQLATLEDRLR.RHEWGLLTIVQPPE
                     LETRIAILKKAQMRLAVPDDVL.ELLASSERNIREGEGALLRVTAPASNKFPIJUK
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                     dna polymerase III beta chain, almost identical to O69590
                     (EMBL:X92504) dnaN (399 aa) (95.98 identity in 353 aa
                     overlap) and highly similar to many eg. DPB3_ECOLI P03035
                     dna polymerase III beta chain (see 2.. (376 aa)
                     fastascores: opt 1324 z-score 1567.3 E(): 0; 52.8%
                     identity in 337 aa overlap overlaps and extends CDS 1.
                     neighboring cosmid MTCY10H4.01"
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                     LPMECGIRVELLGETVVLAATTDFRLAVREE.KWSASSPDIRAAVLVPAKILAAAKRS
                     IGSSLVRLSLEGTSRPGSVKRDGLLSTGNGKRSTRILTRAEFPRFQRLPTEHIIAVVMI
                     VAELLEAIKLVALVADRGAQWMEFADGSVPLSAGADGVGRAAECLVVDTAGSPLTA
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     HTACLKSVPSAARVRGDRGVVDCIEVWDSRLAESGAELVAAKIDIVNQLAPEVKKAYQL
     LAPERSAS2CYRASMDVTGPSEQSDIRQLIAARILAAARRADFENGVCYCLVGVRPH
     RDGLLRLQCPAKGFASHGGEAWSLAVALKLAAYGLLRVDQGEPVLLLDQVFAEDLVM
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     (97.98 identity in 187 aa overlap)"
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     RGRVASVASGRVASRRKSWSGPGCLRCPGFDCKAARELAKKRGWSGVRVAEGMVLGGW
     SAVVGHGINRHARPTALNDGVLSVIAFSTAWATCLRIMQAGLAKIAAAVSNCVVRSD
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     HETTEYDPETVARRLQFMAFLNKEGTIINLTDERVDEVVQEEVDEVSDVAEAPKSASERA
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     GYSESVHTFAN::NTHREGGTHEEGFRSALTSVNKTAKDRKLLKDKCPNLTGDIREG
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     SSAQARIARKAPELVKRKSALDIGGLFGKLADCRSTDPRKSELVVVEGDSAGGSAKS
     GRDSMFQALFPIGKTINERARIDRVIKNTEVQAIIIALGGSSINRDGTFDIGKLRYHKI
     VLMAIAIVGDHISTLILLFHFMRPLIENGVFLAQPELYKLKWGRSHPFAYSCR
     FRCGLEAGLKAGKLNKEDGIGRYKGLGEMDAKELWE2:LMDPSVRVLRQVLLDAAA
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     QEPTVLPSRFPNSLANGSGGINVGMATNIPPHNLRELADAVFWALENHDADEEETLAA
     VMGRVKGPDFPTAGLIVGSQGTADAYKTCRGSIRHMGCVEEVEFDDSRGR8SLVITELPY
     QVNHDNFITSIAEQVRDGK:AGISNIEDQSSDRVGLRIVIEIKRDAVAKVVINNLYKH
     TQLQTSFGANMLAIVDGVVRTLRDQLLRYYVDHQLDVIVRRTIYRLRKANERAHILR
     SKYKALAALDEVIALIRASETVDIARAGLILELLDIDEIQAQAILDMQTRRLAALROR
     IIDDLAK:EAEIADLEDIAKPEKORGIVRDELAEIVDRHGDDRRTRIIAADSGCE
     DLIAREDVVVITEGYNRKIKDLIYRSQKRGGKVGKVGGGALGK.DGIVAHFEVS:HDL
     LATRNG:VKKSLTDFDSNRSGGIVVNLRDNDEIVGAVICSACDDLL:LVSANGGSLR
     FSATDEALRPYGRATSGVQGMRNIDRLISLNVVHEGTYVLVAISCGYAKRIALEEY
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     B1770 (302 aa), FASTA scores: Opt: 812 z-score: 593.0 E():
     1.6e-25, 54.2% identity in 319 aa overlap"
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Query Match
Best Local Similarity   100.0%;
Matches 12732;  Conservative   0;  M.smatches   0;  Indels   0;  Gaps   0;

Qy      1  ACCTGGCGCTTGCAGAGATCAAATAGGGCGCCATGGGCTCAGCCATAGTACAGCTCGTCGCCGCA   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1646015  ACCTGGCGCTTGCAGAGATCAAATAGGGCGCCATGGGCTCAGCCATAGTACAGCTCGTCGCCGCA 1696074

Qy     61  CTTTGATCGATCGGCGAAATAAGCATGTCAGGCAATTAAAAAAGAGAAGCGAGCGACTCGCGG   120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1696075  CTTTGATCGATCGGCGAAATAAGCATGTCAGGGCAATTAAAAAGAGAAGCGCACGGCGACTCGCGG 1696134

Qy    121  CATTCAGCATGTCGAGCCGTCGGTTCGATGTGAGCGCACCATTCCGTTCCAACGATTTCA   180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1696135  CATTCAGCATGTCGAGCCGTCGGTTCGATGTGAGCGCACCATTCCGTTCCAACGATTTCA 1696194

Qy    181  GACCAAGCATTGAATAGTCCACTCGCCGACGTATAICTCGCGCTCCGCGCGATCTATGCGGGGCG   240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1696195  GACGAACCATTGAATAGTCCACTCGCCGACGTATAGTCTCGCGCTCCGATCTATGCGGGGCG 1696254

Qy    241  CCGCAGATGAAGCTCGCTTCGCCCAGCCTTCGCGCGCGCGCGACGACCGCGCATATTCGCGG   300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1696255  CCGCAGATGAAGCTCGCTTCGCCCAGCCTTCGCGCGCGCGCGACGACCGCGCAACATTCGCGG 1696314

Qy    301  CGGGAGAGCGTCGATGCGGCGTGTAATCAGTTTGAAGCGCAGGGCATCGTAGGTAGTCGTA   360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1696315  CGGGGAGAGCGTCGATGCGGCGTGTAATCAGTTTGAAGCGCAGGGCATCGTAGGTAGTCGTA 1696374

Qy    361  GTAGGACGCCATAGGCACAGCCCAGATCGTTGATCGAAAAAGGGTCCGGCGCCCATTGCAAA   420
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Db 1696375  GTAGGACGCCATAGGCACAGCCCAGATCGTTGATCGAAAAAGGGTCCGGCGCCCATTGCAAA 1696434

Qy    421  TGCGGCGACCAGCTGGTCAAAGCGCAACGCCTCCGCTCGCGGTTCCAATCGAGCGATCGT   480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1696435  TGCGGCGACCAGCTGGTCAAAGCGCAACGCCTCCGCTCGCGGTTCCAATCGAGCGATCGT 1696494

Qy    481  GGAGGTCGCCGTCGCGTTGAATTTCGACTGTGTAGTAACGARCCACGTCAGTGAGCATCGT   540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1696495  GGAGGTCGCCGTCGCGTTGAATTTCGACTGTGTAGTAACGAGCCACGTCAGTGAGCATCGT 1696554
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align_1

Qy   2701 GGGATCTTGCCCGA.TGATAGTTCTTGATGCTATCGGTGCAT.AGCAGGAGTGCCTTGCCA 2760
Db 1698725 CGGATCTTGCCCGATTCA.AGTTCTTGA.GCTATCGGGGATCAGTGCAGGAGTGCCTTGCCA 1698774

Qy   2761 AAGGACAACGTTCCCGGGGTGTCGAAAGCCGCCCCGAAGCGAACTA.TGAACTTGATGATCCG 2820
Db 1698775 AAGGACACGTTCCCGGGGTCTCGAAAGCCGCCCCGAAGCGAACTAITGAACTTGATGATCTC 1698834

Qy   2821 TGGATCGACTGTGGATGGTCCCCGGGAGCCTCGTGCCCACAACAGAAAGGCTGCGATA 2880
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Qy   2881 TTGGACACCACCAGCGCGGTGAATCCGGATAACCAGCGCCACCGGGTCCATTGTCGAGCCGCCAAC 2940
Db 1698895 TTGGACACCACC.AGCGCCG.GATCCCGATAGCAGCCCACCGGGTCCATT.CGAGCCCGCTAAC 1698954

Qy   2941 AACACTGACGCCCCAGANACCA.TGAACTSGCGG.TT.ACCA.SGACGGCCAAGACACCGTGCATG 3000
Db 1698955 AACACCACGCCCAGAAGAGNGAGCCGGGTTNAC.BGGACGCCGCAAGACATCA.CTGTGATC 1699014

Qy   3001 STGGCCAGGCGCCCCACCCGTGTCCGGNAA.GGCACACGAGTGAAACCAGCGGGGATAGGTACC 3060
Db 1699015 CBTGGCGAGGCGCCCACGCSGGTGTCCGGAAGGCACACGAGGTAAGCCAGGCGGATCGGTAYC 1699074

Qy   3061 A.GGAACCTTGTCGACTTGCTTGCCTTGCAGCGACTSGGNCCCCCAGCGCGATCGGGCGCCCAAC 3120
Db 1699075 ACGGAAGGCCTGTCCGAGTTGGCGTSGGACTAACGACACGCAAGCTACGGATCGGTATC 1699134

Qy   3121 ASTGT.ACGAGAGAATGACCMCTCTCTCCAGRCCACGTGCCCCNYCGGCCGATCGGTACC 3180
Db 1699135 AGTGTACGAAGATGACCACTCTCTCCCAGAGACACCGTCCCCNGGCCGGCCGAATCGCG 1699194

Qy   3181 GCAGNTAGACCGGCCATCGTTAGSCCGGAC.CAGGTAACAGAACAGCCCAAACGCSGGCCCA 3240
Db 1699195 GGAGATAGAGCCGGCATCGTTAGSGCCGACCAGGTAACAGA.CAGCCCAAAGCCGCGGCCCA 1699254

Qy   3241 CCCAGGCCAATGSTCGGTAGTGAGAAAATGCATACGGTATCGGCGGCGGGGGGCCATGCA 3300
Db 1699255 CCCAGGCCAATGGCTGGGTAGTGCCGAAAATCGCAIACGGTATCGGGCGGGGCCATGCA 1699314

Qy   3301 GCAAACGCGGGTCGGCTGGTAAATCGGGGGTAGCGAGA.TCAAGTAGTCCGCGGGATTGGGT 3360
Db 1699315 GGAACGCGGGTCGGCTGGTAAATCGGCGGGTAGCGAGA.TCAAGTAGTCCGCGGATTGGGT 1699374

Qy   3361 TSAATGCCCGCGGGGGCGGGACCAATGGGGTAGGCGGCGGCTGGGGCCGCGATA.TCATG 3420
Db 1699375 TGAATCCCCGGCGGGTSANCAISGGGTASTGCTGCGAAGGCACGGCGGACCGGATATTCATG 1699434

Qy   3421 CCCCAATCAAGCCMACAGTCCCCAGGGNTTACCCAAAAAGNTIGSAAAGA.GTCGACCGCG 3480
Db 1699435 CCCCAAATCAAGCCMACAGTCGCCCAGGGNTACCCAAAGACT.GGAARAGNCGGCGGACCGGC 1699494

Qy   3481 IAGCACTGACTGAGGGCGTACGCGTCGGGCCCGCGAAATCACCGACCGCAGGGATGCG.G 3540
Db 1699495 TACCACTGACTGAGGGCGTACGCCTCBGCCCCGGGAATCACCGACCGCGACCAGGATGTG 1699554

Qy   3541 CCGAGNTAGGGTGCNCTCCGAATGGGAAGGGCCGATCAGCGCCGCGCTCCGGCTGGG 3600
Db 1699555 CCGAGCTGAGGG:CGCGTCCGAAATGGGAAGCCCAATCACGCGCGGCTCCCGGCTGCG 1699614

Qy   3601 GTCACGGCACGGCGGGCAAGACCCGGGGGGTCGCTTCATCTGGATCTCTCCCGGTTCTGCG 3660
Db 1699675 GTCACGGGCACCCGCGAAACACTCCCGGSGTCCTTCAC.TSGATTCTCCTCGGTTCTGCG 1699674

Qy   3661 CGAAAGGTAGCAGAGCGCCATGGTTGGCAANSGGGTGCCCGSTAGTCTAGACCGGATC 3720
Db 1699675 CGAAACGGTAGCAGAGCGGCCATGGTTGGCAACGCCSGGTSCCCGGGGGTAGTCCAGACCGGATC 1699734

Qy   3721 TTCCTCGTCGGCAACCGACAACACGACGTCGTTGCCGGAAAGGCGGCTGGGCGGCAACGCGG 3780
Db 1699735 PTCCCGGTSGCAACGACAA.ASGGNGG.GTTGCCGGGAAAGGGGCGCAACGCCGAAAGSCTT 1699794

Qy   3781 ACGATGAACCCACAGCTAGCCCCAGGTTATGCCAGGGAAGAGCGACCGGCAGGAGC 3840

Db 1699795 AGGA.GAACCCACNGCACGCCGCCCCGACGGTAGGCGCATGCGGAGAGGCCAGGAGC 1699854

Qy   3841 GGGAACCAGTGAAGCGAAGCCGCCCTCATCACCGGAAGGGAATGCACAGGAGCGGTATTC 3900
Db 1699855 GGGGAACCCAGTGAAGCGCAGCGCCTTCATCACCGGAATCACAGGACGCGGTATCTT 1699914

Qy   3901 GCTAAGGTCCCCGTGAAGGGAATATGTGGCCCGCTGGGTAGCCGCGGACGGTCGTATTC 3960
Db 1699915 GCTAAGGCTCCCCGTGAAGGGGATATGTGGCCCCTGGGTAGCCGCCGGAGGTCTGC 1699974

Qy   4021 AATCACGAATCACCGCGTCACGGGCGAGACATTCATGACTCGTAATCCTCACCATATCGC 4080
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Qy   4081 GGTCGGCAACGGAGGCGGTCGA.CGATGCACGTCTCAGGTTGATCTCGCGGTCAAAGCATCTTGTTC 4140
Db 1700035 GGTCGGCAACGGAGGCGGTCGACGATGCACGTCTCAGGTTGATCTCGCGGTCAAAGCATCTTGTTC 1700094

Qy   4142 TATCAGTATTGGSCCGGTTCCGGCAGCTTACGAGGGGTGATCGGACTCGTAATCCTGTGTT 4200
Db 1700155 TATCAGTAITGGSCGGTTCCGGCAGTCGATGGACTCGTAATCCTGTGTT 1700214

Qy   4201 TCGGTTGAGTAATTAATCTGAACCGTGTGAACCGCATGGATGGAIGGATTCCTTGCCCGTAT 4260
Db 1700215 TCGGTTGAGTAA.AATCTGAACCGTGTGAACCACATGGATGGAIGGATTCCTTGCCCGTAT 1700274

Qy   4261 CCGGTCACATGTTSATGCGCACGGCGGCAAGAAATTGCCTTCACTGTTCGGATACGATGGGCGC 4320
Db 1700275 CCGGTCACATGTTGATGCGGCACGGCGGCAGAATTGCCTTCACTGTTCGGATGATGGGCGGC 1700334

Qy   4321 AITTGCACATCACGCCATCGAGCCCGGACACTGCCTGTCCCGAGGACCTCGCGGCGGTGCCCTGTCGGTGC 4380
Db 1700335 CGAGGCCCGATTTGCACGCGACTGGCTGTCCCGAGGACCTCGGCGGTGCCTGTGTCGGTGC 1700394

Qy   4381 AGCAITGCTGGAAGTGGGCGGSGGGTACTTCTGCTCAGCTGTCAAAGCGGGCAGAGAGGG 4440
Db 1700395 AGCAITGCTGGAAGTGGGCGGSGGGTACTTCTGCTCACGTGACTGGGCGGCGGGAGGG 1700454

Qy   4501 CGACATCGTGCTGGAATTGGGCGCACGAGACCCACCATGGCGCCAICAGGCGGAAAGA 4560
Db 1700455 ATTTGACATCACCGGCCAICGAGCGGCGACGGGTGAAAGGTTTTGGCAAGGCGGGGGGC 1700514

Qy   4561 CGACATCGTGCTGGAATTGGGCGCACGAGACCCACCATGGCGCCAICAGGCGGAAAGA 4560
Db 1700515 CGACATCGTGCTGGAATTGGGCTGCGAGACGACCATCGGCCAGGCGGAAAGA 1700574

Qy   4456: CTTIATTTCCGAGAACGGGTTCGACTTGGCCTTCTGCTCGAAAGTGGATGGAGCACAICGA 4620
Db 1700575 C.TTATTTCCCAGAACGSTTCGACTTGGCTTCTGCTCGAAAGTGATGGAGCACAICGA 1700634

Qy   4681 CTTCCGTGTCGCCGAATTACGTAITACGACGAACGGCATTCAAIATCCCAACATTCTT 4740
Db 1700695 CTTCCGTGTGCCCGGAA.TACGIATTCCCGIACGAACGGCATTCAAIATCCCAACATTCTT 1700754

Qy   4741 CACCAAAAGAGCTGACATCGCCGGGGTGCAICGCACATCGCATGGAGGGCAAIACGGCATGGA 4800
Db 1700755 CACCAAAAGAGCTGACATCGCCGGGGTGCAICGCACATCGCATGGAGGGCAAIACGGCATGGA 1700814

Qy   4801 IGACCCGAAGGGAGCTCGGGSTTCGCTCAACTSGATTACGGGTTCCCAAGGTGNAACGCTT 4860
Db 1700815 IGACCCGAAGGGAGCTCGGGSTTCGCTCAACTSGATTACGGGTTCCCAAGGTGAAACGCTT 1700874

Qy   4861 TCGGGCGAAGGATGCGACGCTGACCTTGGCGCTTGCCACGGCGCAATGTGGTATGGAIGCT 4920

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Db 1696495 GCGGGTGCCGTGTGCTTCGAGTTTCGATGCGTAGTAACGGGCCACGTCAGCGAGCATGGT 1696554

Qy     541 CGTTGCGTCTTCCGCCATGAAGCTGCCTCACGATTTGTGTGTGTGGGCGTCGGTGCGTGG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1696555 CGTTGCGTCTTCCGCCATGAAGCTGCCTCACGATTTGTGTGTGTGGGCGTCGGTGCGTGG 1696614

Qy     601 GTCCGAGACTATACCTTCAACAGTTGCATGCCGAGGCTGCGGCGGGCAATGACCCAAAAA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1696615 GTCCGAGACTATACCTTCAACAGTTGCATGCCGAGGCTGCGGCGGGCAATGACCCAAAAA 1696674

Qy     661 CCCGCCGGCACGGTTCGCCGAGCAAGGAAGCGTGGAGACGATAGATAATTTCACTGGCGA 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1696675 CCCGCCGGCACGGTTCGCCGAGCAAGGAAGCGTGGAGACGATAGATAATTTCACTGGCGA 1696734

Qy     721 CAGTACCTCAAATAGTCCGGAGCCTCGGCTCCGACGTTAAAGAGCAGATCCAGAATCGAC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1696735 CAGTACCTCAAATAGTCCGGAGCCTCGGCTCCGACGTTAAAGAGCAGATCCAGAATCGAC 1696794

Qy     781 ACGGCGGGCTCGAACCCTCCCCACAATTGCTTATAATCGCGGTAGCCGTCATAATCGAAC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1696795 ACGGCGGGCTCGAACCCTCCCCACAATTGCTTATAATCGCGGTAGCCGTCATAATCGAAC 1696854

Qy     841 CAAGTTACCCGGATGCTAAGTTCGTCGAACACGCGCTCATCGACATACGAACGGGCTGAG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1696855 CAAGTTACCCGGATGCTAAGTTCGTCGAACACGCGCTCATCGACATACGAACGGGCTGAG 1696914

Qy     901 GGGCCAGAGACATATTCGGTCGCTGCGGCCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1696915 GGGCCAGAGACATATTCGGTCGCTGCGGCCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 1696974

Qy     961 TTGCCGTCGGCTAATTCGTAGTCCCACGAATTTGCCAGTCGCGTGCTGATACCGAGATAA 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1696975 TTGCCGTCGGCTAATTCGTAGTCCCACGAATTTGCCAGTCGCGTGCTGATACCGAGATAA 1697034

Qy    1021 CTGCAAATCGCATTCAATAGACGGCTGTTGAGTAAGGAAAGATTCGTGTGCTGTTCTTCG 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697035 CTGCAAATCGCATTCAATAGACGGCTGTTGAGTAAGGAAAGATTCGTGTGCTGTTCTTCG 1697094

Qy    1081 AGGTAAATCGGCGCGAGCCAGTCAGCGATCTCCGCAAAATGAGCGGCCCGGCTGTAGTTG 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697095 AGGTAAATCGGCGCGAGCCAGTCAGCGATCTCCGCAAAATGAGCGGCCCGGCTGTAGTTG 1697154

Qy    1141 AATTCTAGTGCCCGCCAGTGCGCTTTCGCCCAATCGGTGCCGTCGATCAGCGTCTCACGT 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697155 AATTCTAGTGCCCGCCAGTGCGCTTTCGCCCAATCGGTGCCGTCGATCAGCGTCTCACGT 1697214

Qy    1201 ATCTTTTGATGGAAACGTCCCTTCACCTGGACGGGAACAGTTATCCACTGTAACCCCTGG 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697215 ATCTTTTGATGGAAACGTCCCTTCACCTGGACGGGAACAGTTATCCACTGTAACCCCTGG 1697274

Qy    1261 CTCGTTTTGATCCGATTTCTGTTTCGCCAATCACGCTTGGTATATTGCATGTCATCATAG 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697275 CTCGTTTTGATCCGATTTCTGTTTCGCCAATCACGCTTGGTATATTGCATGTCATCATAG 1697334

Qy    1321 ATGATGAATTCATCGACGAATGCAATCAGGTCAAAATATCCTCGCCAAGGTATGTAATTT 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697335 ATGATGAATTCATCGACGAATGCAATCAGGTCAAAATATCCTCGCCAAGGTATGTAATTT 1697394

Qy    1381 GATTGAACAATCGCGACTTTCTTCAACGCGGTGTCTCCAATTTAGAATAACAAATACGTC 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697395 GATTGAACAATCGCGACTTTCTTCAACGCGGTGTCTCCAATTTAGAATAACAAATACGTC 1697454

Qy    1441 GCGCCCGCGACAGCTCCGCTGGAGCGAGTTCAAGCGATTCTGCGACATATTCAATATGGT 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697455 GCGCCCGCGACAGCTCCGCTGGAGCGAGTTCAAGCGATTCTGCGACATATTCAATATGGT 1697514

Qy    1501 GCTCGGGAAGGCCAGGATGGCCGGCGACCCGGGGCGTCCGGTGCGCGATGAACGTCGCAT 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697515 GCTCGGGAAGGCCAGGATGGCCGGCGACCCGGGGCGTCCGGTGCGCGATGAACGTCGCAT 1697574

Qy    1561 CGTCTCCTGTGAGATAATTGCATCCGATCATATAGGGCTGGCTGCGGCTAGGTTGCTGGC 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697575 CGTCTCCTGTGAGATAATTGCATCCGATCATATAGGGCTGGCTGCGGCTAGGTTGCTGGC 1697634

Qy    1621 AAAAAGATATCGCGGCCGATCCGTTTCTGGTTTTGTCTTGATGATCAAATCCGCTTCCGT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697635 AAAAAGATATCGCGGCCGATCCGTTTCTGGTTTTGTCTTGATGATCAAATCCGCTTCCGT 1697694

Qy    1681 TCACGAGATCGATTCCTGGTCTTCCCCCAGCGTCGCGATGTCGATAGGTGTCGCGCTTTG 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697695 TCACGAGATCGATTCCTGGTCTTCCCCCAGCGTCGCGATGTCGATAGGTGTCGCGCTTTG 1697754

Qy    1741 TTCGTACCCGCACTACGCGGCGGCGAGAACCTCGCCACCGAATCGGGATTGGGGGAGGA 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697755 TTCGTACCCGCACTACGCGGCGGCGAGAACCTCGCCACCGAATCGGGATTGGGGGAGGA 1697814

Qy    1801 TACCACTCGGTCGAGGCCCGTCACCGGCCTTCTAGCGGGTTGACCATCAGTGTTTGCAGG 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697815 TACCACTCGGTCGAGGCCCGTCACCGGCCTTCTAGCGGGTTGACCATCAGTGTTTGCAGG 1697874

Qy    1861 GCCCTATCCCGGTATGGCGCACCACGGGATCGGCAGCGTTCCGGTTGCTGGCGTGGTACC 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697875 GCCCTATCCCGGTATGGCGCACCACGGGATCGGCAGCGTTCCGGTTGCTGGCGTGGTACC 1697934

Qy    1921 TCGTTGTGGCGCCGTGGTCCATGTCGATTGAGTGCGTGGATCAGTGTAAACCGTTGCGCG 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697935 TCGTTGTGGCGCCGTGGTCCATGTCGATTGAGTGCGTGGATCAGTGTAAACCGTTGCGCG 1697994

Qy    1981 CCATGTTCTGTAGGCACTGGTTCGGGTTGTGGTTAGGCTGCACGGTTGGCAGGTTACCAA 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697995 CCATGTTCTGTAGGCACTGGTTCGGGTTGTGGTTAGGCTGCACGGTTGGCAGGTTACCAA 1698054

Qy    2041 CCACTGAGCCCCTGGGCGGATGTGAGCTCGGACTCCGCCTATGGGGTGTAATTTTGGCAG 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1698055 CCACTGAGCCCCTGGGCGGATGTGAGCTCGGACTCCGCCTATGGGGTGTAATTTTGGCAG 1698114

Qy    2101 ATTGGGCCGGGTCCCCGTGGTGAGGACTCCTCAACCGGATTGGGTAAGCATGAGGTGGTG 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1698115 ATTGGGCCGGGTCCCCGTGGTGAGGACTCCTCAACCGGATTGGGTAAGCATGAGGTGGTG 1698174

Qy    2161 CTGGCAGCGGTGTCCTGGTCGCTCTCCCGAGTAGGCCCGTTGTGACTGTCATGTGGCCGA 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1698175 CTGGCAGCGGTGTCCTGGTCGCTCTCCCGAGTAGGCCCGTTGTGACTGTCATGTGGCCGA 1698234

Qy    2221 GCGGGTTTGCGCGCGTAGGAGACGATGATTACTACGCACGTGACCAACCACAAGAACGGT 2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1698235 GCGGGTTTGCGCGCGTAGGAGACGATGATTACTACGCACGTGACCAACCACAAGAACGGT 1698294

Qy    2281 GCCCATGTCACCGTGGTGAAAACGAGTGGCGTGGTACCGACTACCCCTTTGGCTCCCAGC 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1698295 GCCCATGTCACCGTGGTGAAAACGAGTGGCGTGGTACCGACTACCCCTTTGGCTCCCAGC 1698354

Qy    2341 TGTCCATAGAGCGGCACGTAGAACGGCTGGCCCGGGACCGCGACGTTGACGATGCTCAGC 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1698355 TGTCCATAGAGCGGCACGTAGAACGGCTGGCCCGGGACCGCGACGTTGACGATGCTCAGC 1698414

Qy    2401 GCCACGGCCAAACTCACGCAGACGCCGACCGCGCGGCGGCGGTCTCCATGGGCTGCGAGT 2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1698415 GCCACGGCCAAACTCACGCAGACGCCGACCGCGCGGCGGCGGTCTCCATGGGCTGCGAGT 1698474

Qy    2461 TGGTCGAATATCCCAGCACCAGGAGGCCCGTTGGGGTCTCGGGCTACCAGTGCAGCCATT 2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1698475 TGGTCGAATATCCCAGCACCAGGAGGCCCGTTGGGGTCTCGGGCTACCAGTGCAGCGATT 1698534

Qy    2521 GGCAAGACGAAAACGAGATAGTAGAAGGCGACGTCCGCGGGGGAGAAGGTGGCGGTGGCG 2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1698535 GGCAAGACGAAAACGAGATAGTAGAAGGCGACGTCCGCGGGGGAGAAGGTGGCGGTGGCG 1698594

Qy    2581 AGCAACACAATCCCCACCATGACAGGCGGGATACGGCGTCCGAGCGCCAGCACGGCGACC 2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1698595 AGCAACACAATCCCCACCATGACAGGCGGGATACGGCGTCCGAGCGCCAGCACGGCGACC 169865

Qy    2641 ACGACTATGACTAGGACAGCAAACCCGATCTGCGTTCGCGGACCAGTGAGGAAACCCTCT 27
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1698655 ACGACTATGACTAGGACAGCAAACCCGATCTGCGTTCGCGGACCAGTGAGGAAACC
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Qy   7081  AATCACCGGCCAGGACGGACGGACGGCTCGTATCTCGCCGAATCGC:GCTGG:CAAGGGGTATGAGGC: 7140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703095  AATCACCGGCCAGGACGGACGGACGGCTGTATCTCGCCGAATCGCTGCTGG:CAAGGGGTATGAGGT 1703154

Qy   7141  TCACGGCGCTCATCCGGCGGCGGCCTTCGACGTTCAACGCACCT:CGGGGATCGGATCACCTCTACGT 7200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703155  TCACGGCGCTCATCCGGCGGCGGCCTTCGACGTTCAACGCACCT:CGGGGATCGGATCACCTTACGT 1703214

Qy   7201  CGACCCGGCCACCAACCGGGGGCGGGGCGGTGTTTCTTCCACTATGGTGACCTGACGACGGAAC 7260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703215  CGACCCGGCCACCAACCGGGGGCGGGGCGGTGTTTCTTCCACTATGGTGACCTGACGACGGAAC 1703274

Qy   7261  CCGGTTGGTCGACCCTGCTGACCGACCATCGAACCCGACGAGGGTGTACAAACCTGGCGGGCCA 7320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703275  CCGGTTGGTTGACCCTGCTGACCGACCATCGAACCCGACGAGGGTGTACAAACCTGGCGGGCCA 1703334

Qy   7321  GTCACACGTGCGGGTGACGTTCGACGAACCCGTGCACACCCGGTTGACACCACCCGGCATGGG 7380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703335  GTCACACGTGCGGGTGACGTTCGACGAACCCGTGCACACCCGGTTGACACCACCCGGCATGGG 1703394

Qy   7381  ATCCATGCGACTGCTGCTGGAAGCCGTTCGGCTCTCTCGGGGTGCACTGCGGCTTCT:ATCAGGC: 7440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703395  ATCCATGCGACTGCTGGAAGCCGTTCGGCTCTCTCGGGGTGCACTGCGGCTTCT:ATCAGGC: 1703454

Qy   7441  GTCCTCGTTCGCGGAGATGTTCGGCGGCGCCTGCGCCGCGACCGGCACAGAACGAGCTGACGCGGTTCTA 7500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703455  GTCCTCGTTCGCGGAGATGTTCGGCGGCGCCTGCGCCGCGACCGGCACAGAACGAGCTGACGCGGTTCTA 1703514

Qy   7501  CCCGGGTCACCCIATGGGCGGCGCCCAAGCICTATTCGTACTGCTGGGCGGGCGGCGGCGCCGCAAIATCG 7560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703515  CCCGGGTCACCGIATGGGCGGCGCCCAAGCICTATTCGTACTGCTGGGCGGGCGGCGGCGCCGCAAIATCG 1703574

Qy   7561  CGAAGCGTACGGATTGTTCGGCCGTTAACGGCATCTTGTTCAATCACGAA:CACCGGCGGCG 7620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703575  CGAACCGTACGGATTGTTCGGCCGTTAACGGCATCTGTTCAATCACGAATCACCGGCGGCG 1703634

Qy   7621  CGGTGAGCAGTTIGGTGCACCGGAAGAATCACCACGGCCGGCATCATCAAGCGCCGGTAT 7680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703635  CGGTGAGCAGTTCGTGGTCGTGACCATCGGCAGTCACCAGGGCGGCCGGCATCATCAAGCGCCGGTA: 1703694

Qy   7681  CCAGICCGAGGTCTATATGGGGCAAATCGCCATCGGCCTCCGCGCACTGGGGGTACGGCGCCGA:: 7740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703695  CCAGTCCGAGGTCTATATGGGGCAAATCGCCATCGGCCTCCGCGCACTGGGGGTACGGCGCCGA:: 1703754

Qy   7741  ATACGTCGAAAGCACAITGGGCGGATACTTCGAGCCAGCACGAGCGCAACGACTTCGTTTGGC: 7800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703755  ATACGTCGAAAGCATGTGGCGGAIGTTGTGCAGACCAACCAGAGCGCNGAGTTCGTTTGGC: 1703814

Qy   7801  GACCGGCGCGGGGTTTCACCGTGCGTGACTTCGGGCGGCGCCGGGTTTCGCC:GTCCAGCCA:GCCGGTTT 7860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703815  GACCGGGGCGGGGTTTCACCGTGCGTGACTTCGGGCGGCGCCGGGTTTCGCC:GTCCAGCCA:GCCGGTTT 1703874

Qy   7861  GGACTGCAGCAGTACCGTGAAATDGACCAAGAGCGCIATCTGCGCGGGGCCCACACGAAGTGAC:TC 7920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703875  GGACTGCAGCAGTACGTGAAATCGACCAAGAGCTA:CTGCGCCCCACGAGGTGGAIC 1703934

Qy   7921  GCTGATCGGCGACGGCGGACCAAGGCTGCCCGAATGCTC:GGCTGCGCGCCGCGCTTCGGGCGCACU 7980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703935  GCTGATCGGCGACGGCGGACCGCACCAAGGCTGCCCGAA:TGCTC:GGCTGGGAGGGCTTCGGGCGCACU 1703994

Qy   7981  TGACGAGTTGGCTCTGGGATCATGGTCGACGGGACACAIGGCGGCGCCGCTGGAGTGCCGCGAAGGCAA 8040
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1703995  TGACGAGTTGGCTCTGGGATCATGGTCGACGGGACACAIGGCGGCGCCGCTGGAGTGCCGCGAAGGCAA 1704054

Qy   8041  GCCGTGGAICGGACAAGCCGATGCANGCGGCGACGGATGATCGGGCGAAGGCC 8100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1704055  GCCGTGGATCGGACAAGCCGATGCANGCGGCGACGGATGATCGGGCGAAGGCC 1704114

Qy   8101  CCGCTTGACCCGCCGCGCCCGGGTCTACATCGCGGGCGCTGGTGGGGTCCGCGI 8160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1704115  CCGCTTGACCCGCCGCGGCCCGGGTTACACGCGGGGCA:CGGCGGGGGCTGACGCGCGCTCGGGTCGGCG 1704174

Qy   8161  CTGCTACGCACGTTTGCGGGCGCGGGGGCTTCACCAAGCCGCT:GGTGCGGTGCACGCGCCCAG 8220
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Db 1704175  CTGCTACGCACGTTTGCGGGCGCGGGGGCTTCGCGGGGTT:GACCAAC:GTCGCTCTCGGAGTCGAGGCGGCGCANGGGCGAG 1704234

Qy   8221  CTTGATCGAC3GATCG3GCCCGCGGCGGGGCGG3GGGT:TGACCAACCTCGCTGCGGCGCANGTC 8280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1704235  CTTGACCTGACGGATCG3GCCCGCGGCGGGGCGGCANGGT:TGACCAACCTCGCTGCGGCGCANGTC 1704294

Qy   8281  GTCATCGACGGCGGCGCCCGGGTCGGGCGCCCGGATCCGGCACGAGCACCGGCTACCGGGCGATC 8340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1704295  GTCATCGACGGCGGCGCCCGGGTCGGGCGCCCGGATCCGGCACGAGCACCGGCTACCGGGCGATC 1704354

Qy   8341  TTCGTGCTGGAAAACCTCCAGATCACNGGTCAAGTCGGAGAGCCGGCGTCGGCGCCCGGCGGCGG 8400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1704355  TTCGTGCTGGAAAACCTCCAGATCACNGGTCAAGTCGGAGAGCCGGCGTCGGCGCCCGGCGGCGG 1704414

Qy   8401  GTGCCGCCGCGCTGTGTTCCTGCGTGCTGGCGTGCACTACCGGAAACTGGCGCACTGGGCATC 8460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1704415  GTGCGGCCGCGCTGTGTTCCTGCGGCTGGCGTGCACTACCGGAAACTGGCGCACTGGGCATC 1704474

Qy   8461  ATCCCGGGAGAGCCGGTGCTCACCGGTCCGTTGAGCCGACCAACAGGGCCTGCCGTCGGCGACC 8520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1704475  ATCCCGGGAGAGGCGGGTGCTCACCGGTCCGTTGAGCCGACCAACAGGGCCTGCCGTCGGCGACC 1704534

Qy   8521  GCCAAAATCGCGCGGGCATCCGTTGGGGTCCCAGCGCGCGTCGCGGCGCAACATGGCGCTGTCGGTGG 8580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1704535  GCCAAAATCGCGCGGGCA:CCGTTGCGGTCCCAGCGCGGT3CGGCGGCGACCAACGAGCCGTCGGTGG 1704594

Qy   8581  ACCTCGGCGGA:TGCGCCACAACCTTACGGCGGCCAGCGCGGGGCNCAACTTTTGCGCGTCCGGAACC 8640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1704595  ATCTCGGCGGNTGCGCCACAACCTTACGGCGGCCAGCGCGGT:ACGGGGTGCTGGCACGTCCGGAACC 1704654

Qy   8701  GTGACCAACTGGGGGCACCGGCAGCGCGCACGGNGCCAGTTGCGTGCAGTCGAGCACGACCTGGC3 8760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1704655  CATCTGCTGCGGCACTCATCCGGCGCTATGACGGGCGAAAGCCAGTGGCGGCCGACACTGGGC3 1704714

Qy   8761  AGGCGCAIGCGTGTATCTGCCTGGAACATTGNNNNNCATCTCAAGGTGGAAAC 8820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1704715  GTGACGCAAGTGGGG:ACGGGGACGGACGACTTGCTGCGCGACGACCTGGCG 1704774

Qy   8841  AGGGCATGGACCAGACCGATGGCGGANGAGA:CGGTCGCANTTCANNGCGGNGGNA:GGCGTCGGNTCNGCGCC 8900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1704775  AGGGCATGGACCAGACCGATGGCGGANGA: 1704834

Qy   8941  TCGGTTCTACCGGCAAGTGTCCAATGCTGATGGNNNNTGGN 9000
           ||||||||||||||||||||||||||||||||||||||||
Db 1704835  CGGCATCGACTGGCACGCGNGTGATCGGCATCGGGGGCA:NGGT 1704894

Qy   8961  ACGGTGGCGTGGTTA:CGGCANNGANGGGCGGA:GGTCGGGAATGNGGCTGGCNTTGGCG 9060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1704895  GGCGGAAACGGCTGNTGCIATCGAACCGGGGTCGACG:ANGGGATCGGGGGCA:NGG 1704954

Qy   9061  CTTGGACACAICTTGCGT:GIAACGGACA:CGGAGGCTTNNNGGCTACTIATCGANCT:9:20
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Db 1704955  ACGGTGGCGTGGTTA:CGGCANNNGGGGTCGGTTCNGAACTGGACT 1705034

Qy   9121  GGGAACGAAATTCTTI3GCCAA:TGCAA:TGCAITGAAGGGGACGTGTNGGATAGTAT:CGTC:GAAT 9180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1705035  ACGGTGGCGTGGTTA:CGGCANNNGGGGTCGGTTCNGAACTGGACT 1705094

Qy   9181  CGGCCAATTCGGGCA:AGTA:TGGCA:GGGTCTCGGGCGGCGGGGTTTNGGCGGGG:NGCATCG 9240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1705195  GGGCAATTCGGGCCTTGCCGTCT:TGCACGCGACGGCCTCCACGGACC 9360

Qy   9241  TCTCGTTCGAGTCGCTGCCCGGGGGCCTTTGCCGTCTTCGACGGCGACGGCCTCCACGGACC 9360
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Db 1705259  CGTCGTCGTCGAGCCGGCTGCCCGCGGCCCTTGGCGTCGTGGCGCCCTTGGCGCGTCGTCGGAGTCGCAGCGGCCGCTCCACGGACG 1705354

Qy 9361  CGTCGCGGCAACGCAGGCGCCCGACGCAGTCCCCTTGCCGA  GTTGAAAGGACCANTCAGGACG 9266
Db 1705315  CGTTGTCGGGAATGCCGCCGGCGCGTGTCCGCGGCGGCCGGTCGCATGCAACACTCTCGATCAACG 1705374

Qy 9361  TCGCCGGCAACGCAGGCGCCCGACGCAGTCCCCTTGCCGA GTTGAAAGGACCANTCAGGACG 9426
Db 1705375  TCGGCCGGGAACGCAGGCGCGCCAGCAGTTCCGTCTTGCCGATGTTGAAAGGACACATCAGGAGG 1705434

Qy 9421  CCTTCCACCGCCAACTAGGTGGGCGCCCAACGGGTGCCGATACATCGACTCGATTCCG 9480
Db 1705435  CCTTTCACCAGCCAAACTACGTGGGCGCCCAACGGGTGCCGATACATCGACTCGATCCCG 1705494

Qy 9481  TGGCTGCAGACGTTCTGCCGCGGCCCAACGAGTAATTGCGGTTCTTGAAGATGACGTTCAASGAT 9540
Db 1705495  TGGCTGCAGACGTTCTGCCGCGGCCCAACGGATATTGCGTTCTTGAAGATGACGTTCAASGAT 1705554

Qy 9541  TCGAGAACGCAGGTGA-CGCGCGGGTGGCCAGCTGCACGAGGCTTCAAACGG 9600
Db 1705555  TCGGAGAACAGCAGGTGATCGCGGGGCGGGATTCAAACGGTGCACGAGCCGGATGC 1705614

Qy 9601  AGCTCGGACGTGTCGTTTCCAGCGTTGGTACGGAGGGTCGGCATGTCATCGCGGCAGAGTGCTCG 9660
Db 1705615  AGCTCGGACGTGTCTTTTCCAGCCGTTGTACGGAGGGTCGGCA-GCTCAFCCGGCGAGGGGGCTCG 1705674

Qy 9661  ATCTCGTCGGATTCGTTGGGGTTTTAGGCTCTCGGGGATTGCAACCGGGTTTCACCGGACCCC 9720
Db 1705675  ATCTCGTTGGATTCGTTGGGGTTTACGGCTCTCGGGGATTGCAACCGGGTTTCACCGGACCCC 1705734

Qy 9721  GCAACGGTCGAATGCTGCAGGCCGGATGCATCTCTTCTTCCGGGGGTAGGGATGCTGACGGCGCG 9780
Db 1705735  GCAACGGTCGAATGCTGCAGGCCGGATGCATCTTCTTCCGGGGGCAAGGATTGACGGCGCG 1705794

Qy 9781  GCGGCGTCAATCTTATTTCGACATTTCGCGTGAAGACGTTTCTCCCAGAAATGACTGGTCGTAGG 9840
Db 1705795  GCGGGTCAATCTATTTCGACATTCGCCGTGAAGACGTTTCTCCCAGAATCGACTGTTGTAGG 1705854

Qy 9841  CGTAGAACTCCCGGCGCGGTAGGCGAGGCATGTGATATTTGCGTTCCCGGAACCGGGTAGC 9900
Db 1705855  CGTAGAACTCCCGGCGCGGTAGGTAGGCCATGTGATATTTGCGTTCCCGGAACCGGGTAGC 1705914

Qy 9901  GGCCGATGAAGGGTCGCCCCATCGGCGCCACGAGTCACCCAAAGACCGGCGTTGGTTCCCGTGCG 9960
Db 1705915  GGCGAATGAAGGTCGCCCCATGCGGCGCCAGATCACCCAAAGACCGGCGTTGGTTCCCGTGCG 1705974
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align_1

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Qy  11461  TGTGCCATCACTTGGTTAGGCCC::CGGGTGGTTCCTGGGTTTGTTCGACATGGTCAGGCTC  11520
Db 1707475  TGTGCCATCACTTGGTTAGGCCC::CGGG:TGGCTCCTGGGTTTGTTCGACATGGTCAGGCTC 1707534
Qy  11521  GACAGCGCGCGTCGGAGCGGAGAGGGCCACACATCCAGGAGCGCCCTGCGGCTCGGCGCTGC  11580
Db 1707535  GACAGCGCGGGTCGGAGCGCG:GGAGGGCCACACATCCAGGAGCGCCCTGCGGCTCGGCGCGC 1707594
Qy  11581  CGGCGGCGAGCGTTCGGCCACTGGGCGTTCAGGCGCGGCGCGGGTGCGCCGGGGTGCT  11640
Db 1707595  CGGCGGCGAGCGTTCGGCCA::TGGGGTTTCAGGCGCG::G:GCGGCGGTGCGGCCGGGGTGCT 1707654
Qy  11641  GCAGCGGCCAGCATGGGCGATC:GAGGATGGGCGCGGCGGATGGTTGCGTCCAGGCGGGCGGCGCC  11700
Db 1707655  GCAGCGGCCAGCATGGGCGATC:GAGGATGGGCGCGGCGGATGGTTGCGTCCAGGCGGGCGGCGCC 1707714
Qy  11701  CGTCCCGGGGCCTGGAAGTTGGGCGATCTGGCCGAAGGATCCACG::CGGCCATGGGCCGGCGATGA  11760
Db 1707715  CGTCCCGGGGCTGGAAGCTGGGGATCTGGCCGAAGGATCCACG::CGGCCATGGGCCGGCGATGA 1707774
Qy  11761  GTCTCCTCGGCGCGGGGGGGTCTCCCGGGAAC:ACGTCGAGCATCGGCATGCCGT:GAAAGCGTGCCGGCAT  11820
Db 1707775  GTCTCCTCGGCGCGGGGGGGTCTCCCGGGAAC:ACGTCGAGCATCGGCATGCCGT:GAAAGCGTGCCGGCAT 1707834
Qy  11821  GCCCCGGCGACCCTGGCGTCAACCAGAAC:TTGGCGGGTCCACCCACCTGGTTCTGTCGGCGCATCC  11880
Db 1707835  GCCCCGGCGACCCTGGCGTCAACCAGAACTTGGCGGGTCCACCCACCTGGTTCTGTCGGCGCATCC 1707894
Qy  11881  CTTGGCGCGTCGGCGGGGGATACACGGGCCATGGTGTCGCGGCCACATGGCGATGC:GGCCATGCA  11940
Db 1707895  CTTGGCGCGTCGGCGGGGATACACGGGCCATGGTGTCGCGGCCACATGGCGATGC:GGCCATGCA 1707954
Qy  11941  CCGCGTGCCGACG:GCAGA:ACCATCCACAGGGCGATGA:GTCGGCAGGAAATGTCCTCGTT  12000
Db 1707955  CCGCGTGCCGACG:GCAGA:ACCATCCACAGGGCGATGA:GTCGGCAGGAAATGTCCTCGTT 1708014
Qy  12001  ACCGCGTCGAAGCGACGGTACAGCGGTACG:GCGCA:GTTGGTCTGGA:GAAGTTCATCAAGAATCAACG  12060
Db 1708015  ACCGCGTCGAAGCGACGGTACAGCGGTACG:GCGCA:GTTGGTCTGGA:GAAGTTCATCAAGAATCAACG 1708074
Qy  12061  CATCCAGGCTTCAACTTCGCGCGG:AACCGCAGGGGAACTTGCTGTCTGATGAAGTTCATCAAGAATCAACG  12120
Db 1708075  CATCCAGGCTTCAACTTCGCGCGG:AACCGCAGGGGAACTTGCTGTCTGATGAAGTTCGAGTCCTTGGCATGGC 1708134
Qy  12121  CGTCCCGGCATATCACTCGGCACGGGATCGGAAAG:CACCGGTCGTCTTGGCGTCGGCGGTCGA  12180
Db 1708135  CGTCCCGGCATATCACTCGGCACGGGATCGGAAAG:CACCGGTCGTCTTGGCGTCGGCGGTCGA 1708194
Qy  12181  GGAATCCGCGACCTGTTTGGTTAGCTTCAGCGGATCGATCGAGTANGTCGGCCTCGGCCACA  12240
Db 1708195  GGAATCCGCGACCTGTTTGGTTAGCTTCGGCGATCGATCGAGTANGTCGGCCTCGGCCACA 1708254
Qy  12241  AGGCGACGTA::CGCCCGCAGCCGCGCAGCAGCGGCGGCGGGGTCCAGGTTCCCATTCGAGGCCGA  12300
Db 1708255  ACGGCGACGTA::CGCCCGCAGCCGCGCAGCAGCGGCGGCGGGGTCCAGGTTCCCATTCGAGGCCGA 1708314
Qy  12301  GGTT:CGGTCTCGAAGATGCACGGGATCGAGCGAA:CACGCTGGTTGGGGTGGGCCGGTCCGACAGGA  12360
Db 1708315  GGTT:CGGTCTCGAAGATGCACGGGATCGAGCGAA:CACGCTGGTTGGGGTGGGCCGGTCCGACAGGA 1708374
Qy  12361  TGCATCGGCGGTCGGTCGGGCAATCGGTCGGCTCCGGGCGA:SGGATGATCTCGCACGGGCGGAAGT  12420
Db 1708375  TGCATCGGCGGTCGGTCGGGCAATCGGTCGGCTCCGGGCGA:SGGATGATCTCGCACGGGCGGAAGT 1708434
Qy  12421  GGTT:CGCTCGTGCCGAGAAAGCCTCTCGAACGCCTGACCGGGTCAGGGATCACGCCGACCGTTCCTG  12480
Db 1708435  TGGTCGAGACGA:GAGATGCTCACGCTCGGGCGACT:CACCGTCGCGCCGCCGGTTCCGGCAGTCGA:GTC 1708494
Qy  12481  TGGTTCGAGACGA:GAGATGCTCACGCTCGGGCGACT:CACCGTCGCGCCGCCGGTTCCTG  12540
Db 1708495  CGCGGCGGCCAGAGGGTATSGCGATGGCGAAGGTGAATSGCCTSGGCGGATCGCGAGGGCGGTSGC 1708554
Qy  12541  CGCGGCGGCCAGAGGGTATSGCGATGGCGAAGGTGAATSGCCTSGGCGGATCGCGAGGGCGGTSGC  12600
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Db 1708555  CGCGGCGCGCAAGGGTATTCGGCGGTATTCGGATGGCGGCACGGGGCGCGGAAGTAGGCAGGGTGC  1708614
Qy   1261  CGTCGTGGCCTGGTGGTCTCGGCGGACGTACGGCACACGGGGCAAGTAGGCAGGGTGC  1320
Db 1708615  CGTCGTGGCCTGGTGGTCGGCGGACGTACGGCACACGGGCCGGAAGTAGGCAGGGTGC  1708674
Qy   1261  ACTGACGTTGGGCCTCGAACGCGCGGCGCGTSGGGTSGTGGGGCGACCGTCTCGAGTCGGTGC  1320
Db 1708675  ACTGA:CGTTGGGCGTCGAACCSCGTSGCGCGGCGTSGGGGCGACCGTSGGGCGCCACCGTCTCGAGTCGGTSGC  1708734
Qy  12721  TGGTTGGGTCGGC  12732
Db 1708735  TGGTTGGGTCGGC  1708746
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RESULT 2